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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/655,272

DATE: 06/15/2001
TIME: 17:23:49

Input Set : A:\138300.app
Output Set: N:\CRF3\06152001\I655272.raw

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3 <110> APPLICANT: HONORE, ERIC
4 FINK, MICHEL
5 LAZDUNSKI, MICHEL
6 LESAGE, FLORIAN
7 DUPRAT, FABRICE
9 <120> TITLE OF INVENTION: MECHANOSENSITIVE MAMMALIAN POTASSIUM CHANNELS
10 ACTIVATABLE BY POLYUNSATURATED FATTY ACIDS AND THE USE
11 OF SAID CHANNELS IN DRUG SCREENING
13 <130> FILE REFERENCE: 1383-00
15 <140> CURRENT APPLICATION NUMBER: 09/655,272
16 <141> CURRENT FILING DATE: 2000-09-05
18 <150> PRIOR APPLICATION NUMBER: PCT/FR99/00404
19 <151> PRIOR FILING DATE: 1999-02-23
21 <150> PRIOR APPLICATION NUMBER: FR 98/02725
22 <151> PRIOR FILING DATE: 1998-03-05
24 <160> NUMBER OF SEQ ID NOS: 5
26 <170> SOFTWARE: PatentIn Ver. 2.1
28 <210> SEQ ID NO: 1
29 <211> LENGTH: 1757
30 <212> TYPE: DNA
31 <213> ORGANISM: Unknown Sequence
33 <220> FEATURE:
34 <221> NAME/KEY: CDS
35 <222> LOCATION: (284)..(1477)
37 <220> FEATURE:
38 <223> OTHER INFORMATION: Description of Unknown Sequence: DNA encoding TRAAK
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45 acttcacgtc gacccttctc tgagtcttct gccactcact ggcctggaca agacagcatt 180
47 ggggagccca gaggctgcag gtgcagtgac cactgctccc caggagctcc ctgctccttc 240
49 ttcccaggca ggaagtggag ctggacctgc ctctggaagg acc atg cgc agc acc 295
50 Met Arg Ser Thr
51 1
53 aca ctc ctg gct ctg ctg gca ctg gtg ctg ctt tac ttg gta tct ggg 343
54 Thr Leu Leu Ala Leu Leu Ala Leu Val Leu Leu Tyr Leu Val Ser Gly
55 5 10 15 20
57 gct cta gtg ttc cag gct ctg gag cag cct cac gag cag gct cag 391
58 Ala Leu Val Phe Gln Ala Leu Glu Gln Pro His Glu Gln Gln Ala Gln
59 25 30 35
61 aag aaa atg gat cat ggc cga gac cag ttt ctg agg gac cat ccc tgt 439
62 Lys Lys Met Asp His Gly Arg Asp Gln Phe Leu Arg Asp His Pro Cys
63 40 45 50
65 gtg agc cag aag agc ctg gag gat ttc atc aag ctc ctg gtt gaa gcc 487
66 Val Ser Gln Lys Ser Leu Glu Asp Phe Ile Lys Leu Leu Val Glu Ala
67 55 60 65
69 ctg gga ggg ggc gca aac cca gaa acc agc tgg acc aat agc agc aac 535

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70 Leu Gly Gly Gly Ala Asn Pro Glu Thr Ser Trp Thr Asn Ser Ser Asn
71      70      75      80
73 cac tca tca gct tgg aac ctg ggc agc gcc ttc ttt ttc tcg ggg acc 583
74 His Ser Ser Ala Trp Asn Leu Gly Ser Ala Phe Phe Ser Gly Thr
75 85      90      95      100
77 atc atc act acc atc ggc tat ggc aat ata gtc tta cac aca gat gcc 631
78 Ile Ile Thr Thr Ile Gly Tyr Gly Asn Ile Val Leu His Thr Asp Ala
79      105      110      115
81 ggg cgt ctc ttt tgt atc ttc tat gca ctg gtg ggg atc cca ctg ttc 679
82 Gly Arg Leu Phe Cys Ile Phe Tyr Ala Leu Val Gly Ile Pro Leu Phe
83      120      125      130
85 ggg atg ctg ctg gcg gga gtc ggg gac cgg ctg ggc tcc tct ctg cgc 727
86 Gly Met Leu Leu Ala Gly Val Gly Asp Arg Leu Gly Ser Ser Leu Arg
87      135      140      145
89 cgg ggc atc ggc cac atc gaa gca atc ttc ttg aag tgg cat gtg cca 775
90 Arg Gly Ile Gly His Ile Glu Ala Ile Phe Leu Lys Trp His Val Pro
91      150      155      160
93 ccg ggg ctg gtg aga agt ctg tcc gca gtg ctc ttc ctg ctg atc ggc 823
94 Pro Gly Leu Val Arg Ser Leu Ser Ala Val Leu Phe Leu Leu Ile Gly
95 165      170      175      180
97 tgc ctg ctc ttt gtc ctc act cct acc ttc gtg ttc tcc tac atg gag 871
98 Cys Leu Leu Phe Val Leu Thr Pro Thr Phe Val Phe Ser Tyr Met Glu
99      185      190      195
101 agc tgg agc aag tta gaa gcc atc tac ttt gtt ata gtg act ctc acc 919
102 Ser Trp Ser Lys Leu Glu Ala Ile Tyr Phe Val Ile Val Thr Leu Thr
103      200      205      210
105 act gta ggc ttt ggc gat tat gta ccc ggc gat ggc acc ggg cag aac 967
106 Thr Val Gly Phe Gly Asp Tyr Val Pro Gly Asp Gly Thr Gly Gln Asn
107      215      220      225
109 tct cca gcc tac cag ccg ctg gtg tgg ttc tgg atc ttg ttt ggc cta 1015
110 Ser Pro Ala Tyr Gln Pro Leu Val Trp Phe Trp Ile Leu Phe Gly Leu
111      230      235      240
113 gcc tac ttc gcc tca gtg ctc acc acc atc ggc aac tgg ttg cga gca 1063
114 Ala Tyr Phe Ala Ser Val Leu Thr Thr Ile Gly Asn Trp Leu Arg Ala
115 245      250      255      260
117 gtg tcc cgc cga act cgg gca gag atg ggt ggc cta acg gca cag gct 1111
118 Val Ser Arg Arg Thr Arg Ala Glu Met Gly Gly Leu Thr Ala Gln Ala
119      265      270      275
121 gct agc tgg acc ggc aca gtg aca gcg cga gtg acc cag cga act ggg 1159
122 Ala Ser Trp Thr Gly Thr Val Thr Ala Arg Val Thr Gln Arg Thr Gly
123      280      285      290
125 ccc agc gcc ccg ccg cca gag aag gag caa cca ctc ctg ccc tcc tct 1207
126 Pro Ser Ala Pro Pro Pro Glu Lys Glu Gln Pro Leu Leu Pro Ser Ser
127      295      300      305
129 ttg ccg gca ccg cct gct gtt gtt gag cca gcc ggc agg ccc ggc tcc 1255
130 Leu Pro Ala Pro Pro Ala Val Val Glu Pro Ala Gly Arg Pro Gly Ser
131      310      315      320
133 cct gca ccc gca gag aag gtt gag act ccg tcc ccg ccc acg gcc tca 1303
134 Pro Ala Pro Ala Glu Lys Val Glu Thr Pro Ser Pro Pro Thr Ala Ser

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135 325          330          335          340
137 gct ctg gat tac ccc agt gag aat ctg gcc ttc atc gac gag tcc tca 1351
138 Ala Leu Asp Tyr Pro Ser Glu Asn Leu Ala Phe Ile Asp Glu Ser Ser
139          345          350          355
141 gac acg cag agt gag cgt ggc tgt gcc ctg cct cgg gct cct cgg ggt 1399
142 Asp Thr Gln Ser Glu Arg Gly Cys Ala Leu Pro Arg Ala Pro Arg Gly
143          360          365          370
145 cgc cgc cga ccc aac cca tcc aaa aag cct tcc aga ccc cgg ggt cct 1447
146 Arg Arg Arg Pro Asn Pro Ser Lys Lys Pro Ser Arg Pro Arg Gly Pro
147          375          380          385
149 ggg cga ctc cga gac aag gcc gtg ccg gtg taggggcagg atctctggac 1497
150 Gly Arg Leu Arg Asp Lys Ala Val Pro Val
151          390          395
153 ccg gatccca cgc cagggt ttc gctcttg ctgatgctca ggc atgcttg gcttatttga 1557
155 ccaaagagcc gtcctcttt tgttccacgt ggttgcaacc ctgacaggag tccagtgggt 1617
157 gccaatgcc accgctcttc cctggctggg tcttcacatc caatcatttc caaagcccac 1677
159 catccaaggc tttctgcctc gctcccctgc cggttttgac cctcacacct cacaactgtg 1737
161 cctcaaaacc tgcaccaata 1757
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165 <211> LENGTH: 398
166 <212> TYPE: PRT
167 <213> ORGANISM: Unknown Sequence
169 <220> FEATURE:
170 <223> OTHER INFORMATION: Description of Unknown Sequence: TRAAK
172 <400> SEQUENCE: 2
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174 1 5 10 15
176 Leu Val Ser Gly Ala Leu Val Phe Gln Ala Leu Glu Gln Pro His Glu
177 20 25 30
179 Gln Gln Ala Gln Lys Lys Met Asp His Gly Arg Asp Gln Phe Leu Arg
180 35 40 45
182 Asp His Pro Cys Val Ser Gln Lys Ser Leu Glu Asp Phe Ile Lys Leu
183 50 55 60
185 Leu Val Glu Ala Leu Gly Gly Gly Ala Asn Pro Glu Thr Ser Trp Thr
186 65 70 75 80
188 Asn Ser Ser Asn His Ser Ser Ala Trp Asn Leu Gly Ser Ala Phe Phe
189 85 90 95
191 Phe Ser Gly Thr Ile Ile Thr Thr Ile Gly Tyr Gly Asn Ile Val Leu
192 100 105 110
194 His Thr Asp Ala Gly Arg Leu Phe Cys Ile Phe Tyr Ala Leu Val Gly
195 115 120 125
197 Ile Pro Leu Phe Gly Met Leu Leu Ala Gly Val Gly Asp Arg Leu Gly
198 130 135 140
200 Ser Ser Leu Arg Arg Gly Ile Gly His Ile Glu Ala Ile Phe Leu Lys
201 145 150 155 160
203 Trp His Val Pro Pro Gly Leu Val Arg Ser Leu Ser Ala Val Leu Phe
204 165 170 175
206 Leu Leu Ile Gly Cys Leu Leu Phe Val Leu Thr Pro Thr Phe Val Phe
207 180 185 190

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209 Ser Tyr Met Glu Ser Trp Ser Lys Leu Glu Ala Ile Tyr Phe Val Ile
210      195      200      205
212 Val Thr Leu Thr Thr Val Gly Phe Gly Asp Tyr Val Pro Gly Asp Gly
213      210      215      220
215 Thr Gly Gln Asn Ser Pro Ala Tyr Gln Pro Leu Val Trp Phe Trp Ile
216 225      230      235      240
218 Leu Phe Gly Leu Ala Tyr Phe Ala Ser Val Leu Thr Thr Ile Gly Asn
219      245      250      255
221 Trp Leu Arg Ala Val Ser Arg Arg Thr Arg Ala Glu Met Gly Gly Leu
222      260      265      270
224 Thr Ala Gln Ala Ala Ser Trp Thr Gly Thr Val Thr Ala Arg Val Thr
225      275      280      285
227 Gln Arg Thr Gly Pro Ser Ala Pro Pro Pro Glu Lys Glu Gln Pro Leu
228      290      295      300
230 Leu Pro Ser Ser Leu Pro Ala Pro Pro Ala Val Glu Pro Ala Gly
231 305      310      315      320
233 Arg Pro Gly Ser Pro Ala Pro Ala Glu Lys Val Glu Thr Pro Ser Pro
234      325      330      335
236 Pro Thr Ala Ser Ala Leu Asp Tyr Pro Ser Glu Asn Leu Ala Phe Ile
237      340      345      350
239 Asp Glu Ser Ser Asp Thr Gln Ser Glu Arg Gly Cys Ala Leu Pro Arg
240      355      360      365
242 Ala Pro Arg Gly Arg Arg Arg Pro Asn Pro Ser Lys Lys Pro Ser Arg
243      370      375      380
245 Pro Arg Gly Pro Gly Arg Leu Arg Asp Lys Ala Val Pro Val
246 385      390      395
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250 <211> LENGTH: 336
251 <212> TYPE: PRT
252 <213> ORGANISM: Unknown Sequence
254 <220> FEATURE:
255 <223> OTHER INFORMATION: Description of Unknown Sequence: TWIK
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261 His Arg Ser Ala Trp Cys Phe Gly Phe Leu Val Leu Gly Tyr Leu Leu
262      20      25      30
264 Tyr Leu Val Phe Gly Ala Val Val Phe Ser Ser Val Glu Leu Pro Tyr
265      35      40      45
267 Glu Asp Leu Leu Arg Gln Glu Leu Arg Lys Leu Lys Arg Arg Phe Leu
268      50      55      60
270 Glu Glu His Glu Cys Leu Ser Glu Gln Gln Leu Glu Gln Phe Leu Gly
271 65      70      75      80
273 Arg Val Leu Glu Ala Ser Asn Tyr Gly Val Ser Val Leu Ser Asn Ala
274      85      90      95
276 Ser Gly Asn Trp Asn Trp Asp Phe Thr Ser Ala Leu Phe Phe Ala Ser
277      100      105      110
279 Thr Val Leu Ser Thr Thr Gly Tyr Gly His Thr Val Pro Leu Ser Asp
280      115      120      125

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282 Gly Gly Lys Ala Phe Cys Ile Ile Tyr Ser Val Ile Gly Ile Pro Phe
283      130      135      140
285 Thr Leu Leu Phe Leu Thr Ala Val Val Gln Arg Ile Thr Val His Val
286 145      150      155      160
288 Thr Arg Arg Pro Val Leu Tyr Phe His Ile Arg Trp Gly Phe Ser Lys
289      165      170      175
291 Gln Val Val Ala Ile Val His Ala Val Leu Leu Gly Phe Val Thr Val
292      180      185      190
294 Ser Cys Phe Phe Phe Ile Pro Ala Ala Val Phe Ser Val Leu Glu Asp
295      195      200      205
297 Asp Trp Asn Phe Leu Glu Ser Phe Tyr Phe Cys Phe Ile Ser Leu Ser
298      210      215      220
300 Thr Ile Gly Leu Gly Asp Tyr Val Pro Gly Glu Gly Tyr Asn Gln Lys
301 225      230      235      240
303 Phe Arg Glu Leu Tyr Lys Ile Gly Ile Thr Cys Tyr Leu Leu Leu Gly
304      245      250      255
306 Leu Ile Ala Met Leu Val Val Leu Glu Thr Phe Cys Glu Leu His Glu
307      260      265      270
309 Leu Lys Lys Phe Arg Lys Met Phe Tyr Val Lys Lys Asp Lys Asp Glu
310      275      280      285
312 Asp Gln Val His Ile Ile Glu His Asp Gln Leu Ser Phe Ser Ser Ile
313      290      295      300
315 Thr Asp Gln Ala Ala Gly Met Lys Glu Asp Gln Lys Gln Asn Glu Pro
316 305      310      315      320
318 Phe Val Ala Thr Gln Ser Ser Ala Cys Val Asp Gly Pro Ala Asn His
319      325      330      335
322 <210> SEQ ID NO: 4
323 <211> LENGTH: 370
324 <212> TYPE: PRT
325 <213> ORGANISM: Unknown Sequence
327 <220> FEATURE:
328 <223> OTHER INFORMATION: Description of Unknown Sequence: TREK
330 <400> SEQUENCE: 4
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334 Lys Pro Arg Leu Ser Phe Ser Ser Lys Pro Thr Val Leu Ala Ser Arg
335      20      25      30
337 Val Glu Ser Asp Ser Ala Ile Asn Val Met Lys Trp Lys Thr Val Ser
338      35      40      45
340 Thr Ile Phe Leu Val Val Val Leu Tyr Leu Ile Ile Gly Ala Ala Val
341      50      55      60
343 Phe Lys Ala Leu Glu Gln Pro Gln Glu Ile Ser Gln Arg Thr Thr Ile
344 65      70      75      80
346 Val Ile Gln Lys Gln Thr Phe Ile Ala Gln His Ala Cys Val Asn Ser
347      85      90      95
349 Thr Glu Leu Asp Glu Leu Ile Gln Gln Ile Val Ala Ala Ile Asn Ala
350      100      105      110
352 Gly Ile Ile Pro Leu Gly Asn Ser Ser Asn Gln Val Ser His Trp Asp
353      115      120      125

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VERIFICATION SUMMARY

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